

O'Bryen, Barbara

From: Switzer, Juliet
Sent: Friday, December 17, 2004 2:37 PM
To: O'Bryen, Barbara
Subject: FW: search request

see below.

please search in all nucleic acid prior art databases and return results on disk.
thanks.

-----Original Message-----

From: Spencer, Mark
Sent: Friday, December 17, 2004 2:36 PM
To: Switzer, Juliet
Subject: RE: search request

Juliet,

Send a search request to the STIC biotech with a note to the searcher to contact me to get the CD. I will give the searcher the CD and they will copy and paste the sequence into their search system.

Thanks,
Mark

-----Original Message-----

From: Switzer, Juliet
Sent: Friday, December 17, 2004 2:29 PM
To: Spencer, Mark
Subject: search request

hi mark,

I need a search of seq id no 1 of 09/925065. The CRFE in the case says to contact you because the sequence listing is not in the database.

thanks.

Juliet

RESULT 1
AB045146
LOCUS AB045146 27870 bp DNA linear PRI 22-AUG-2000
DEFINITION Homo sapiens TPMT gene for thiopurine S-methyltransferase, complete cds.
ACCESSION AB045146
VERSION AB045146.1 GI:8777468
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Nakamura,Y.
TITLE Genomic structure of Thiopurine S-methyltransferase gene
JOURNAL Published Only in DataBase (2000)
REFERENCE 2 (bases 1 to 27870)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2000) Yusuke Nakamura, Human Genome Center, Institute of Medical Science, The University of Tokyo, Laboratory of Molecular Medicine; Shirokanedai 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:kumikok@ims.u-tokyo.ac.jp, Tel:81-03-5449-5375, Fax:81-03-5449-5406)
FEATURES
source Location/Qualifiers
1. .27870
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6p22.3"
/country="Japan"
gene join(6816. .6955,8033. .8125,12221. .12353,16234. .16286,16914. .16988,22064. .22149,23779. .23823,25177. .25289)
/gene="TPMT"
CDS join(6816. .6955,8033. .8125,12221. .12353,16234. .16286,16914. .16988,22064. .22149,23779. .23823,25177. .25289)
/gene="TPMT"
/codon_start=1
/product="thiopurine S-methyltransferase"
/protein_id="BAA97037.1"
/db_xref="GI:8777469"
/translation="MDGTRTSLDIEEYSDETVQKNQVLTLEEWQDKWVNGKTAFAHQEQ
GHQLLKKHLDFTFLKGKSGLRVFFPLCGKAVEMKWFADRGHSVVGVEISELGIQEFFTE
QNLSYSEEPITEIPGTVFKSSSGNISLYCCSIFDLPRTNIGKFDMIWDRGALVAINP
GDRKCYADTMFSLLGKKFQYLLCVLSYDPTKHPGPPFYVPHAEIERLFGKICNIRCLE
KVDAFEERHKSWGIDCLFEKLYLLTEK"

ORIGIN

Query Match 99.5%; Score 437.6; DB 9; Length 27870;
Best Local Similarity 98.6%; Pred. No. 5.6e-83;
Matches 434; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGAGAGTGTAGTGAGCCAAGATTGTGCCCTGCACTCCAGCGTGGGTAACAGAGTGAGA 60
||:|:|||||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24093 CARARAGTGTAGTKAGCCAARATTGTGCCMCTGCACTCCAGCGTGGGTAACAGAGTGAGA 24152
Qy 61 CTCCATCTAAAAAAAAAAAAACCTATTGTGAACTATTAGTATATTAGTATCTAGAGTATGT 120

Db	24153	 CTCCATCTAAAAAAAAAAAAACCTATTGTGAACATTAGTATATTAGTATCTAGAGTATGT	24212
Qy	121	CTATAAAATTTAAAAGATAAAAGACCATTTTATTGAAAGTTGTTTTATCTTAGAAAAGGAA	180
Db	24213	 CTATAAAATTTAAAAGATAAAAGACCATTTTATTGAAAGTTGTTTTATCTTAGAAAAGGAA	24272
Qy	181	CTAATCTCTGTAAATATGCTCTGTRTATATGCTATATGCTCTATGTTAAAGGTATTTGAA	240
Db	24273	 CTAATCTCTGTAAATATGCTCTGTATATATGCTATATGCTCTATGTTAAAGGTATTTGAA	24332
Qy	241	CTTTTCTAGAGAGATGGTATATATTTTTTTTATTTGTTTATTTTTGAGATAGGATCTTGAT	300
Db	24333	 CTTTTCTAGAGAGATGGTATATATTTTTTTTATTTGTTTATTTTTGAGATAGGATCTTGAT	24392
Qy	301	CTGTCACCCAGGCTGGAGTACAGAAGTGCAATCACAGCTCACTGCAGCCTCGACCTCCCT	360
Db	24393	 CTGTCACCCAGGCTGGAGTACAGAAGTGCAATCACAGCTCACTGCAGCCTCGACCTCCCT	24452
Qy	361	GGGCACAAGTGATCCTCCCACCTCAGCCTCCCAAGTTTCTGGGACCAGAGGCATGCACCA	420
Db	24453	 GGGCACAAGTGATCCTCCCACCTCAGCCTCCCAAGTTTCTGGGACCAGAGGCATGCACCA	24512
Qy	421	CAATGCTTAGCTAATTTTTTC	440
Db	24513	 CAATGCTTAGCTAATTTTTTC	24532

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 03:59:11 ; Search time 3313 Seconds
 (without alignments)
 6280.552 Million cell updates/sec

Title: US-09-925065A-SEQ1
 Perfect score: 440
 Sequence: 1 cagagagtgtagtgtgagccaa.....caatgcttagctaatttttc 440

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_ba:*
 2: gb_htg:*
 3: gb_in:*
 4: gb_om:*
 5: gb_ov:*
 6: gb_pat:*
 7: gb_ph:*
 8: gb_pl:*
 9: gb_pr:*
 10: gb_ro:*
 11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
c	1	437.6	99.5	27870	9	AB045146			AB045146 Homo sapi
	2	436.4	99.2	147927	9	AL589723			AL589723 Human DNA
	3	359.6	81.7	170346	2	AC145821			AC145821 Papio anu
	4	159.8	36.3	185353	9	AL162732			AL162732 Human DNA

c	5	153.4	34.9	164310	2	AC016156	AC016156	Homo sapi
c	6	153.4	34.9	205834	9	AP006193	AP006193	Homo sapi
	7	151	34.3	198410	2	AP000831	AP000831	Homo sapi
	8	148.6	33.8	181086	9	AL133215	AL133215	Human DNA
	9	148.6	33.8	215103	2	AC058821	AC058821	Homo sapi
	10	148.2	33.7	203230	2	AC026346	AC026346	Homo sapi
	11	148	33.6	149374	2	AC053520	AC053520	Homo sapi
	12	148	33.6	175754	9	AC084018	AC084018	Homo sapi
c	13	147.8	33.6	44024	9	AC133963	AC133963	Homo sapi
	14	147.4	33.5	33026	9	AF156673	AF156673	Homo sapi
	15	147.4	33.5	177893	9	AC005089	AC005089	Homo sapi
	16	147	33.4	179262	9	AL355343	AL355343	Human DNA
c	17	147	33.4	184778	2	AC023567	AC023567	Homo sapi
	18	146.4	33.3	108893	9	AC079169	AC079169	Homo sapi
	19	146.2	33.2	184515	9	AC010653	AC010653	Homo sapi
c	20	146	33.2	179155	9	AL353748	AL353748	Human DNA
c	21	145.2	33.0	181466	2	AC137089	AC137089	Homo sapi
c	22	145	33.0	87507	9	AC132006	AC132006	Homo sapi
	23	145	33.0	148260	2	AC068498	AC068498	Homo sapi
	24	144.8	32.9	171364	9	AL359844	AL359844	Human DNA
	25	144.6	32.9	153803	2	AC055722	AC055722	Homo sapi
	26	144.4	32.8	182078	2	AC140904	AC140904	Homo sapi
c	27	143	32.5	78816	2	AC145755	AC145755	Pan trogl
c	28	143	32.5	201659	2	AC146419	AC146419	Pan trogl
	29	142.6	32.4	131329	9	AC004873	AC004873	Homo sapi
c	30	142.6	32.4	156630	9	BS000087	BS000087	Pan trogl
c	31	142.6	32.4	157435	9	HS50024	AL034380	Human DNA
c	32	142.6	32.4	163914	9	AC098487	AC098487	Homo sapi
	33	142.6	32.4	189319	9	AL158154	AL158154	Human DNA
c	34	142.6	32.4	315681	2	AL355380	AL355380	Homo sapi
c	35	142.4	32.4	198333	9	BS000088	BS000088	Pan trogl
c	36	142.2	32.3	99701	9	AC109319	AC109319	Homo sapi
c	37	142.2	32.3	103097	9	AL445464	AL445464	Human DNA
c	38	142.2	32.3	118484	9	AY268350	AY268350	Homo sapi
c	39	142.2	32.3	135162	9	HS451B21	AL033522	Human DNA
	40	142.2	32.3	143614	2	AC025147	AC025147	Homo sapi
	41	142.2	32.3	158500	2	AL359206	AL359206	Homo sapi
	42	142.2	32.3	161678	2	AC009337	AC009337	Homo sapi
	43	142.2	32.3	175132	9	AC008134	AC008134	Homo sapi
	44	142.2	32.3	178328	2	AC019265	AC019265	Homo sapi
	45	142.2	32.3	179375	2	AC092971	AC092971	Homo sapi

Run on: December 22, 2004, 03:59:06 ; Search time 407 Seconds
 (without alignments)
 5675.050 Million cell updates/sec

Title: US-09-925065A-SEQ1
 Perfect score: 440
 Sequence: 1 cagagagtgtagttagccaa.....caatgcttagctaatttttc 440

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result		Query							
No.	Score	Match	Length	DB	ID			Description	
c	1	137	31.1	98865	6	ABQ78054		Abq78054 Human Ras	
	2	136.2	31.0	114693	8	AAD48308		Aad48308 Human tra	
	3	133.8	30.4	10515	6	ABK10772		Abk10772 Human sma	
	4	133	30.2	118384	10	ABX56555		Abx56555 Human aut	
c	5	132.4	30.1	46340	3	ABN97978		Abn97978 Human ret	
c	6	131.4	29.9	190117	10	ADL13780		Adl13780 Osteoarth	
c	7	131	29.8	52216	4	AAH28355		Aah28355 Nucleotid	
c	8	131	29.8	52216	6	ABL50307		Abl50307 Human mus	
	9	130.8	29.7	190117	10	ADL13780		Adl13780 Osteoarth	
	10	130.2	29.6	110000	5	AAF84800		Aaf84800 Nucleotid	
	11	129.8	29.5	49806	9	ADB16927		Adb16927 Human DYX	
	12	129.6	29.5	22013	4	AAK85635		Aak85635 Human imm	

	13	129.6	29.5	22013	5	ABA16084	Abal6084 Human ner
	14	129.6	29.5	22026	4	AAK85636	Aak85636 Human imm
	15	129.6	29.5	22026	5	ABA16085	Abal6085 Human ner
	16	129.6	29.5	175737	6	ABK83571	Abk83571 Human cDN
	17	129.6	29.5	175737	10	ADL13596	Adl13596 Osteoarth
	18	129.6	29.5	175737	12	ADQ18934	Adq18934 Human sof
C	19	129.4	29.4	119950	2	AAX90201	Aax90201 Human yes
	20	128.6	29.2	52216	4	AAH28355	Aah28355 Nucleotid
	21	128.6	29.2	52216	6	ABL50307	Ab150307 Human mus
C	22	128.4	29.2	96593	11	ADL27146	Adl27146 Human gen
C	23	128.4	29.2	96595	9	ADA03068	Ada03068 Human PPP
C	24	128.4	29.2	96595	10	ADB72806	Adb72806 Human PPP
C	25	128.4	29.2	96596	9	ADA66352	Ada66352 Human PPP
	26	127.8	29.0	17335	4	ABK42393	Abk42393 Genomic s
	27	127.8	29.0	17335	9	ADB60549	Adb60549 Connectiv
	28	127.8	29.0	19882	4	ABK42394	Abk42394 Genomic s
	29	127.8	29.0	19882	9	ADB60550	Adb60550 Connectiv
	30	127.8	29.0	86765	10	ADD14752	Add14752 Human src
C	31	127.4	29.0	12392	5	ABA15896	Abal5896 Human ner
C	32	127.4	29.0	166181	12	ADQ20461	Adq20461 Human sof
C	33	127.4	29.0	166181	12	ADQ18633	Adq18633 Human sof
	34	127	28.9	176001	12	ADK43203	Adk43203 Human pro
	35	127	28.9	186739	12	ADK43195	Adk43195 Human pro
	36	126.8	28.8	7385	4	AAH72843	Aah72843 Human cer
C	37	126.4	28.7	94719	10	ADE95902	Ade95902 Human STA
C	38	126.4	28.7	94720	9	ADA02654	Ada02654 Human STA
C	39	126.4	28.7	94720	10	ADB72392	Adb72392 Human STA
	40	126	28.6	8855	5	ABA19146	Abal19146 Human ner
	41	126	28.6	51474	5	AAF97846	Aaf97846 Human neu
C	42	125.8	28.6	57296	4	AAK78847	Aak78847 Human imm
C	43	125.8	28.6	57296	4	AAK78170	Aak78170 Human imm
C	44	125.8	28.6	57296	4	AAK79364	Aak79364 Human imm
C	45	125.8	28.6	57296	4	AAK86799	Aak86799 Human imm

Run on: December 22, 2004, 04:17:56 ; Search time 93 Seconds
 (without alignments)
 3362.872 Million cell updates/sec

Title: US-09-925065A-SEQ1
 Perfect score: 440
 Sequence: 1 cagagagtgtagttagccaa.....caatgcttagctaatttttc 440

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
c	1	125.8	28.6	319608	4	US-09-539-333D-1		Sequence 1, Appli
c	2	125.8	28.6	319608	4	US-09-679-409-1		Sequence 1, Appli
c	3	123.4	28.0	44848	4	US-09-435-739-42		Sequence 42, Appl
c	4	123.4	28.0	44848	4	US-09-988-113-42		Sequence 42, Appl
	5	123.2	28.0	246240	2	US-08-724-394A-20		Sequence 20, Appl
	6	123.2	28.0	246240	2	US-08-724-394A-21		Sequence 21, Appl
	7	123.2	28.0	246240	2	US-08-724-394A-22		Sequence 22, Appl
c	8	120.2	27.3	54550	4	US-10-327-189-42		Sequence 42, Appl
c	9	117.6	26.7	12597	4	US-09-705-299-12		Sequence 12, Appl
	10	117.6	26.7	30350	4	US-10-118-328-3		Sequence 3, Appli
c	11	117.2	26.6	29629	4	US-09-729-995-3		Sequence 3, Appli
c	12	117.2	26.6	29629	4	US-10-135-689-3		Sequence 3, Appli
	13	116.8	26.5	90541	4	US-09-759-359A-3		Sequence 3, Appli
	14	116.8	26.5	90541	4	US-10-207-973-3		Sequence 3, Appli
c	15	116.6	26.5	33769	4	US-09-544-398B-8		Sequence 8, Appli
c	16	116.6	26.5	33769	4	US-09-543-771-8		Sequence 8, Appli
c	17	116.2	26.4	246240	2	US-08-724-394A-20		Sequence 20, Appl
c	18	116.2	26.4	246240	2	US-08-724-394A-21		Sequence 21, Appl

c	19	116.2	26.4	246240	2	US-08-724-394A-22	Sequence 22, Appl
	20	115.6	26.3	307	4	US-09-513-999C-29011	Sequence 29011, A
	21	114.8	26.1	6678	3	US-08-816-617A-1	Sequence 1, Appli
c	22	114.8	26.1	98844	4	US-09-791-211-10	Sequence 10, Appl
	23	114.6	26.0	75395	4	US-09-984-890-3	Sequence 3, Appli
	24	114.6	26.0	75395	4	US-10-274-194-3	Sequence 3, Appli
	25	114	25.9	64467	4	US-09-803-671B-3	Sequence 3, Appli
c	26	113.6	25.8	54945	4	US-09-967-669-10	Sequence 10, Appl
	27	113	25.7	46718	4	US-09-816-093-3	Sequence 3, Appli
c	28	112.2	25.5	53332	4	US-09-801-861-3	Sequence 3, Appli
c	29	112.2	25.5	53332	4	US-10-224-562-3	Sequence 3, Appli
	30	112.2	25.5	70000	4	US-09-851-896-3	Sequence 3, Appli
c	31	111.6	25.4	30350	4	US-10-118-328-3	Sequence 3, Appli
c	32	111.6	25.4	43950	3	US-09-735-934A-3	Sequence 3, Appli
c	33	111.6	25.4	43950	4	US-10-060-332-3	Sequence 3, Appli
c	34	111.6	25.4	43950	4	US-10-339-657-3	Sequence 3, Appli
c	35	111.6	25.4	64467	4	US-09-803-671B-3	Sequence 3, Appli
	36	111.2	25.3	13158	2	US-08-687-080-105	Sequence 105, App
c	37	111.2	25.3	55298	4	US-09-491-356C-1	Sequence 1, Appli
	38	110.6	25.1	63000	4	US-09-780-172-18	Sequence 18, Appl
c	39	110.6	25.1	116592	4	US-09-818-512-3	Sequence 3, Appli
c	40	110.4	25.1	619	4	US-09-152-060-17	Sequence 17, Appl
	41	110.4	25.1	84495	3	US-09-797-906-3	Sequence 3, Appli
	42	109.8	25.0	29485	4	US-09-785-381-6	Sequence 6, Appli
	43	109.8	25.0	55298	4	US-09-491-356C-1	Sequence 1, Appli
c	44	109.8	25.0	81001	4	US-09-750-580-1	Sequence 1, Appli
	45	109.8	25.0	107820	4	US-09-792-616-1	Sequence 1, Appli

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 04:18:16 ; Search time 4686 Seconds
(without alignments)
518.389 Million cell updates/sec

Title: US-09-925065A-SEQ1
Perfect score: 440
Sequence: 1 cagagagtgtagtgcacaa.....caatgcttagctaatttttc 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

	No.	Score	Match	Length	DB	ID	Description
c	1	152.4	34.6	667	13	US-10-027-632-19561	Sequence 19561, A
c	2	152.4	34.6	667	15	US-10-027-632-19561	Sequence 19561, A
c	3	140.2	31.9	2393	13	US-10-027-632-102715	Sequence 102715,
c	4	140.2	31.9	2393	15	US-10-027-632-102715	Sequence 102715,
c	5	140.2	31.9	2394	13	US-10-027-632-111593	Sequence 111593,
c	6	140.2	31.9	2394	13	US-10-027-632-111594	Sequence 111594,
c	7	140.2	31.9	2394	15	US-10-027-632-111593	Sequence 111593,
c	8	140.2	31.9	2394	15	US-10-027-632-111594	Sequence 111594,
c	9	137	31.1	98865	9	US-09-770-689A-3	Sequence 3, Appli
	10	136.2	31.0	114693	18	US-10-473-392-3	Sequence 3, Appli
c	11	132.8	30.2	430442	18	US-10-417-375-128	Sequence 128, App
c	12	132.6	30.1	52745	17	US-10-741-601-5726	Sequence 5726, Ap
	13	132.4	30.1	161334	13	US-10-087-192-730	Sequence 730, App
c	14	132.2	30.0	1011	13	US-10-027-632-253775	Sequence 253775,
c	15	132.2	30.0	1011	15	US-10-027-632-253775	Sequence 253775,
c	16	131	29.8	52216	9	US-09-747-810-1	Sequence 1, Appli
	17	129.8	29.5	50000	15	US-10-364-505-7	Sequence 7, Appli
	18	129.8	29.5	50000	17	US-10-681-199-7	Sequence 7, Appli
c	19	128.8	29.3	104062	13	US-10-087-192-916	Sequence 916, App
c	20	128.6	29.2	43173	13	US-10-087-192-2026	Sequence 2026, Ap
	21	128.6	29.2	52216	9	US-09-747-810-1	Sequence 1, Appli
c	22	128.4	29.2	96595	15	US-10-034-650-34	Sequence 34, Appl
	23	127.8	29.0	17335	9	US-09-764-847-1280	Sequence 1280, Ap
	24	127.8	29.0	17335	14	US-10-092-154-1280	Sequence 1280, Ap
	25	127.8	29.0	19882	9	US-09-764-847-1281	Sequence 1281, Ap
	26	127.8	29.0	19882	14	US-10-092-154-1281	Sequence 1281, Ap
	27	127	28.9	176001	16	US-10-210-556-27	Sequence 27, Appl
	28	127	28.9	186739	16	US-10-210-556-19	Sequence 19, Appl
c	29	126.4	28.7	94720	16	US-10-052-482-160	Sequence 160, App
c	30	125.8	28.6	160921	13	US-10-087-192-1672	Sequence 1672, Ap
c	31	125.8	28.6	319608	15	US-10-147-603-1	GENERAL INFORMATI
c	32	125.2	28.5	21739	17	US-10-741-601-5713	Sequence 5713, Ap
	33	125.2	28.5	37940	15	US-10-348-073A-12	Sequence 12, Appl
	34	125.2	28.5	38000	15	US-10-175-627-11	Sequence 11, Appl
c	35	125	28.4	50000	15	US-10-364-505-7	Sequence 7, Appli
c	36	125	28.4	50000	17	US-10-681-199-7	Sequence 7, Appli
c	37	124.8	28.4	46130	15	US-10-017-161-985	Sequence 985, App
	38	124.8	28.4	55611	15	US-10-017-161-783	Sequence 783, App
	39	124.6	28.3	24446	17	US-10-741-601-5740	Sequence 5740, Ap
c	40	124.6	28.3	389182	13	US-10-087-192-1102	Sequence 1102, Ap
	41	124.4	28.3	21913	10	US-09-764-891-6065	Sequence 6065, Ap
	42	124.4	28.3	21913	10	US-09-764-891-6066	Sequence 6066, Ap
	43	124.4	28.3	21913	10	US-09-764-891-6067	Sequence 6067, Ap
c	44	124.4	28.3	54000	10	US-09-843-377-11	Sequence 11, Appl
c	45	124.4	28.3	54000	17	US-10-819-244-11	Sequence 11, Appl

OM nucleic - nucleic search, using sw model

Run on: December 22, 2004, 04:16:31 ; Search time 2965 Seconds
 (without alignments)
 5407.582 Million cell updates/sec

Title: US-09-925065A-SEQ1
 Perfect score: 440
 Sequence: 1 cagagagtgtagtgcgacaa.....caatgcttagctaatttttc 440

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	136.6	31.0	596	7	CN274384	CN274384 170006000
c	2	135.2	30.7	660	8	AQ013712	AQ013712 RPCI11-23
	3	133	30.2	3868	3	BC033908	BC033908 Homo sapi
c	4	132.2	30.0	582	6	CD696556	CD696556 EST13079
	5	131.8	30.0	571	4	BM826251	BM826251 K-EST0098
	6	130.2	29.6	553	5	BQ100951	BQ100951 ij22b01.y
c	7	130.2	29.6	557	7	CK819114	CK819114 if08b12.x
	8	130.2	29.6	560	4	BM128002	BM128002 if08b12.y
c	9	130.2	29.6	563	4	BM127735	BM127735 if08b12.x

	10	130.2	29.6	565	7	CK819115	CK819115	if08b12.y
c	11	130.2	29.6	566	5	BQ102328	BQ102328	ij20b06.x
	12	130.2	29.6	573	5	BQ086237	BQ086237	ij20b06.y
	13	130.2	29.6	592	7	CK823027	CK823027	ij22b01.y
c	14	130.2	29.6	616	5	BQ004314	BQ004314	UI-H-EI0-
	15	130.2	29.6	645	6	CB128065	CB128065	K-EST0177
	16	130.2	29.6	676	4	BI828537	BI828537	603078424
c	17	128.6	29.2	562	7	CK823026	CK823026	ij22b01.x
c	18	128.4	29.2	534	8	B86133	B86133	RPCI11-22C1
c	19	127.2	28.9	444	4	BI481343	BI481343	H2RPE-163
	20	127.2	28.9	651	5	BX488111	BX488111	DKFZp686E
c	21	126.6	28.8	666	9	AG073023	AG073023	Pan trogl
	22	125.4	28.5	6146	8	AQ839831	AQ839831	260L13-C4
c	23	123.4	28.0	666	9	AG167441	AG167441	Pan trogl
c	24	123.2	28.0	513	2	AW973217	AW973217	EST385315
c	25	123.2	28.0	660	8	BZ603692	BZ603692	WHADP18TR
c	26	123.2	28.0	1003	4	BM542339	BM542339	AGENCOURT
	27	123	28.0	565	1	AA577885	AA577885	nn25d10.s
	28	122.8	27.9	351	1	AI014347	AI014347	am51g08.s
c	29	122.8	27.9	515	5	BX479862	BX479862	DKFZp686P
	30	122.8	27.9	656	5	BU681280	BU681280	UI-CF-EC1
c	31	122.2	27.8	309	1	AA533823	AA533823	nj94b10.s
	32	122	27.7	688	6	CA426034	CA426034	UI-H-DF0-
	33	122	27.7	699	4	BI871115	BI871115	603394292
c	34	122	27.7	706	9	AG121314	AG121314	Pan trogl
	35	122	27.7	780	7	CN431118	CN431118	170005999
c	36	122	27.7	1281	3	AF130056	AF130056	Homo sapi
	37	121.8	27.7	443	1	AI278802	AI278802	qo42d10.x
c	38	121.6	27.6	379	1	AA179163	AA179163	zp12d02.s
	39	121.6	27.6	476	8	AQ735338	AQ735338	HS_3024_B
c	40	121.2	27.5	770	5	BX953657	BX953657	DKFZp7810
	41	120.8	27.5	390	8	B03790	B03790	cSRL-187d7-
c	42	120.6	27.4	670	9	AG056372	AG056372	Pan trogl
c	43	120.4	27.4	356	2	AW834135	AW834135	MR2-TT001
c	44	120.4	27.4	356	2	AW834160	AW834160	MR2-TT001
	45	120.4	27.4	479	5	BX089489	BX089489	BX089489